

GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 11, 2006, 22:41:25 ; Search time 189.875 Seconds  
(without alignments)  
458.231 Million cell updates/sec

Title: US-10-072-159-1  
Perfect score: 31  
Sequence: 1 FXXXXXXXXXXXXXXXXXXXXXGXYXFX 31

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10072159/runat\_10082006\_161645\_23320/app\_query.fasta\_1  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=1000 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=100  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss08 -USER=US10072159@CGN\_1\_1\_252@runat\_10082006\_161645\_23320  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%		Query			
No.	Score	Match	Length	DB	ID	Description	
c	1	23	74.2	758	5	US-09-974-300-2197	Sequence 2197, Ap
c	2	23	74.2	888	3	US-09-937-862B-23	Sequence 23, Appl
	3	23	74.2	1206	3	US-09-543-681A-1133	Sequence 1133, Ap
	4	23	74.2	2101	4	US-10-094-749-1399	Sequence 1399, Ap
c	5	23	74.2	3219	3	US-09-614-221A-470	Sequence 470, App
c	6	22	71.0	377	3	US-09-621-976-11394	Sequence 11394, A
c	7	22	71.0	505	3	US-09-533-559-1234	Sequence 1234, Ap
c	8	22	71.0	525	3	US-09-949-016-5412	Sequence 5412, Ap
	9	22	71.0	601	3	US-09-949-016-48909	Sequence 48909, A
	10	22	71.0	601	3	US-09-949-016-48910	Sequence 48910, A
	11	22	71.0	601	3	US-09-949-016-49081	Sequence 49081, A
	12	22	71.0	601	3	US-09-949-016-49082	Sequence 49082, A
	13	22	71.0	601	3	US-09-949-016-49253	Sequence 49253, A
	14	22	71.0	601	3	US-09-949-016-49254	Sequence 49254, A
	15	22	71.0	601	3	US-09-949-016-49429	Sequence 49429, A
	16	22	71.0	601	3	US-09-949-016-49430	Sequence 49430, A
c	17	22	71.0	601	3	US-09-949-016-151201	Sequence 151201,
	18	22	71.0	601	3	US-09-949-016-160930	Sequence 160930,
c	19	22	71.0	601	3	US-09-949-016-177580	Sequence 177580,
	20	22	71.0	700	3	US-09-735-271-217	Sequence 217, App
c	21	22	71.0	714	3	US-09-270-767-3438	Sequence 3438, Ap
c	22	22	71.0	714	3	US-09-270-767-18720	Sequence 18720, A
c	23	22	71.0	726	3	US-09-533-559-5611	Sequence 5611, Ap
c	24	22	71.0	794	3	US-09-533-559-6598	Sequence 6598, Ap
c	25	22	71.0	801	3	US-09-252-991A-1475	Sequence 1475, Ap
	26	22	71.0	801	3	US-09-710-279-2065	Sequence 2065, Ap
	27	22	71.0	807	3	US-09-252-991A-1702	Sequence 1702, Ap
	28	22	71.0	879	3	US-09-134-001C-1305	Sequence 1305, Ap
	29	22	71.0	918	3	US-09-328-352-1943	Sequence 1943, Ap
	30	22	71.0	1083	3	US-09-270-767-6118	Sequence 6118, Ap
	31	22	71.0	1083	3	US-09-270-767-21400	Sequence 21400, A
c	32	22	71.0	1178	3	US-09-270-767-29091	Sequence 29091, A
c	33	22	71.0	1215	3	US-08-952-899-3	Sequence 3, Appli
	34	22	71.0	1215	3	US-09-328-352-4056	Sequence 4056, Ap
c	35	22	71.0	1332	3	US-08-952-899-1	Sequence 1, Appli
c	36	22	71.0	1479	3	US-09-248-796A-4621	Sequence 4621, Ap
c	37	22	71.0	1485	2	US-07-702-771-2	Sequence 2, Appli
c	38	22	71.0	1485	2	US-08-438-883-2	Sequence 2, Appli
c	39	22	71.0	1485	2	US-08-741-599-2	Sequence 2, Appli
c	40	22	71.0	1514	3	US-08-675-816-1	Sequence 1, Appli
	41	22	71.0	1530	3	US-09-248-796A-5928	Sequence 5928, Ap
	42	22	71.0	2069	3	US-09-276-438-8	Sequence 8, Appli
c	43	22	71.0	2103	3	US-09-270-767-13179	Sequence 13179, A
c	44	22	71.0	2229	3	US-10-104-047-450	Sequence 450, App
c	45	22	71.0	2312	2	US-07-736-178C-1	Sequence 1, Appli
c	46	22	71.0	2685	2	US-08-935-450-5	Sequence 5, Appli
c	47	22	71.0	2685	3	US-09-338-123-5	Sequence 5, Appli
c	48	22	71.0	3191	3	US-08-675-816-3	Sequence 3, Appli
	49	22	71.0	4043	3	US-09-710-279-3354	Sequence 3354, Ap

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OM protein - protein search, using sw model

Run on: August 11, 2006, 08:01:40 ; Search time 34.875 Seconds  
(without alignments)  
77.805 Million cell updates/sec

Title: US-10-072-159-1  
Perfect score: 31  
Sequence: 1 FXXXXXXXXXXXXXXXXXXXXXGXFXFX 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	71.0	266	2	US-09-710-279-2066	Sequence 2066, Ap
2	22	71.0	268	2	US-09-252-991A-18273	Sequence 18273, A
3	22	71.0	292	2	US-09-134-001C-4142	Sequence 4142, Ap
4	22	71.0	305	2	US-09-328-352-6069	Sequence 6069, Ap
5	22	71.0	404	2	US-09-328-352-8182	Sequence 8182, Ap
6	21	67.7	156	2	US-09-198-452A-698	Sequence 698, App
7	21	67.7	156	2	US-09-438-185A-662	Sequence 662, App
8	21	67.7	201	1	US-08-801-740-6	Sequence 6, Appli
9	21	67.7	201	1	US-08-801-740-7	Sequence 7, Appli
10	21	67.7	201	2	US-08-801-740-6	Sequence 6, Appli

11	21	67.7	201	2	US-08-801-740-7	Sequence 7, Appli
12	21	67.7	252	2	US-09-252-991A-30813	Sequence 30813, A
13	21	67.7	270	2	US-09-902-540-13092	Sequence 13092, A
14	21	67.7	450	2	US-09-489-039A-10052	Sequence 10052, A
15	21	67.7	1233	2	US-09-134-000C-4971	Sequence 4971, Ap
16	21	67.7	1416	2	US-09-071-035-404	Sequence 404, App
17	21	67.7	1416	2	US-10-206-576-404	Sequence 404, App
18	21	67.7	1448	2	US-09-071-035-402	Sequence 402, App
19	21	67.7	1448	2	US-10-206-576-402	Sequence 402, App
20	20	64.5	63	1	US-08-637-759B-501	Sequence 501, App
21	20	64.5	63	2	US-08-871-355A-501	Sequence 501, App
22	20	64.5	63	2	US-09-201-945-501	Sequence 501, App
23	20	64.5	63	2	US-09-714-602-501	Sequence 501, App
24	20	64.5	86	2	US-09-178-093B-34	Sequence 34, Appl
25	20	64.5	110	2	US-09-270-767-44692	Sequence 44692, A
26	20	64.5	142	1	US-08-997-080-47	Sequence 47, Appl
27	20	64.5	142	1	US-08-997-362-47	Sequence 47, Appl
28	20	64.5	142	2	US-08-873-970-47	Sequence 47, Appl
29	20	64.5	142	2	US-09-095-855-47	Sequence 47, Appl
30	20	64.5	142	2	US-08-705-347A-47	Sequence 47, Appl
31	20	64.5	142	2	US-09-324-542-47	Sequence 47, Appl
32	20	64.5	142	2	US-09-205-426-47	Sequence 47, Appl
33	20	64.5	142	2	US-09-200-643-47	Sequence 47, Appl
34	20	64.5	143	2	US-08-685-808-2	Sequence 2, Appli
35	20	64.5	143	2	US-08-505-860C-2	Sequence 2, Appli
36	20	64.5	162	1	US-08-606-143-44	Sequence 44, Appl
37	20	64.5	226	2	US-09-270-767-44619	Sequence 44619, A
38	20	64.5	229	2	US-09-270-767-56999	Sequence 56999, A
39	20	64.5	312	2	US-09-543-681A-5883	Sequence 5883, Ap
40	20	64.5	329	2	US-09-248-796A-16263	Sequence 16263, A
41	20	64.5	336	2	US-08-987-691A-5	Sequence 5, Appli
42	20	64.5	408	2	US-09-252-991A-33131	Sequence 33131, A
43	20	64.5	421	2	US-10-012-231A-234	Sequence 234, App
44	20	64.5	421	2	US-10-015-389A-234	Sequence 234, App
45	20	64.5	421	2	US-10-006-768A-234	Sequence 234, App
46	20	64.5	421	2	US-10-015-671A-234	Sequence 234, App
47	20	64.5	421	2	US-10-015-393A-234	Sequence 234, App
48	20	64.5	421	2	US-10-011-833A-234	Sequence 234, App
49	20	64.5	421	2	US-10-006-041A-234	Sequence 234, App
50	20	64.5	421	2	US-10-012-064A-234	Sequence 234, App
51	20	64.5	421	2	US-10-015-392A-234	Sequence 234, App
52	20	64.5	421	3	US-10-011-795B-234	Sequence 234, App
53	20	64.5	421	3	US-10-015-386A-234	Sequence 234, App
54	20	64.5	421	3	US-10-012-121A-234	Sequence 234, App
55	20	64.5	421	3	US-10-006-485A-234	Sequence 234, App
56	20	64.5	421	3	US-10-006-746A-234	Sequence 234, App
57	20	64.5	421	3	US-10-012-752A-234	Sequence 234, App
58	20	64.5	421	3	US-10-017-253A-234	Sequence 234, App
59	20	64.5	421	3	US-10-015-519A-234	Sequence 234, App
60	20	64.5	421	3	US-10-015-715A-234	Sequence 234, App
61	20	64.5	421	3	US-10-007-236A-234	Sequence 234, App
62	20	64.5	429	2	US-09-922-501-10	Sequence 10, Appl
63	20	64.5	448	2	US-09-361-443-4	Sequence 4, Appli
64	20	64.5	451	2	US-09-902-540-15200	Sequence 15200, A
65	20	64.5	462	2	US-09-583-110-3587	Sequence 3587, Ap
66	20	64.5	467	2	US-09-361-443-2	Sequence 2, Appli
67	20	64.5	469	2	US-09-198-452A-793	Sequence 793, App

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OM protein - protein search, using sw model

Run on: August 11, 2006, 08:18:16 ; Search time 195.3 Seconds  
(without alignments)  
73.526 Million cell updates/sec

Title: US-10-072-159-1  
Perfect score: 31  
Sequence: 1 FXXXXXXXXXXXXXXXXXXXXXGXFXFX 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	22	71.0	119	4	US-10-434-156-17	Sequence 17, Appl
2	22	71.0	136	4	US-10-434-156-22	Sequence 22, Appl
3	22	71.0	163	3	US-09-030-847-2	Sequence 2, Appli
4	22	71.0	163	4	US-10-215-088-2	Sequence 2, Appli
5	22	71.0	163	4	US-10-775-165-2	Sequence 2, Appli
6	22	71.0	215	3	US-09-030-847-4	Sequence 4, Appli
7	22	71.0	215	4	US-10-215-088-4	Sequence 4, Appli
8	22	71.0	215	4	US-10-170-385-289	Sequence 289, App
9	22	71.0	215	4	US-10-775-165-4	Sequence 4, Appli
10	22	71.0	219	4	US-10-276-774-2150	Sequence 2150, Ap
11	22	71.0	266	5	US-10-793-626-2066	Sequence 2066, Ap

12	22	71.0	278	5	US-10-732-923-858	Sequence 858, App
13	22	71.0	292	4	US-10-724-972A-4167	Sequence 4167, Ap
14	22	71.0	296	4	US-10-282-122A-67003	Sequence 67003, A
15	22	71.0	302	4	US-10-282-122A-77397	Sequence 77397, A
16	22	71.0	374	4	US-10-437-963-159816	Sequence 159816,
17	22	71.0	440	6	US-11-087-099-5856	Sequence 5856, Ap
18	22	71.0	636	4	US-10-425-114-68352	Sequence 68352, A
19	22	71.0	636	4	US-10-425-115-274242	Sequence 274242,
20	22	71.0	1421	4	US-10-424-599-275109	Sequence 275109,
21	22	71.0	1678	4	US-10-437-963-126095	Sequence 126095,
22	22	71.0	1730	4	US-10-424-599-275110	Sequence 275110,
23	22	71.0	3705	4	US-10-282-122A-77944	Sequence 77944, A
24	21	67.7	53	4	US-10-029-386-29069	Sequence 29069, A
25	21	67.7	71	4	US-10-425-115-272794	Sequence 272794,
26	21	67.7	71	4	US-10-425-115-279228	Sequence 279228,
27	21	67.7	79	4	US-10-424-599-240256	Sequence 240256,
28	21	67.7	83	4	US-10-424-599-168732	Sequence 168732,
29	21	67.7	100	4	US-10-425-115-364312	Sequence 364312,
30	21	67.7	107	6	US-11-096-568A-16598	Sequence 16598, A
31	21	67.7	128	4	US-10-466-242-51	Sequence 51, Appl
32	21	67.7	131	4	US-10-767-701-42874	Sequence 42874, A
33	21	67.7	150	4	US-10-437-963-154089	Sequence 154089,
34	21	67.7	156	4	US-10-289-762-698	Sequence 698, App
35	21	67.7	156	4	US-10-282-122A-54708	Sequence 54708, A
36	21	67.7	156	4	US-10-425-115-333955	Sequence 333955,
37	21	67.7	158	4	US-10-425-115-333946	Sequence 333946,
38	21	67.7	158	6	US-11-096-568A-16597	Sequence 16597, A
39	21	67.7	165	4	US-10-425-114-44317	Sequence 44317, A
40	21	67.7	201	3	US-09-833-245-2073	Sequence 2073, Ap
41	21	67.7	201	3	US-09-833-245-2075	Sequence 2075, Ap
42	21	67.7	201	3	US-09-833-245-2076	Sequence 2076, Ap
43	21	67.7	201	4	US-10-039-865-6	Sequence 6, Appli
44	21	67.7	201	4	US-10-039-865-7	Sequence 7, Appli
45	21	67.7	201	4	US-10-060-255-59	Sequence 59, Appl
46	21	67.7	201	4	US-10-060-255-68	Sequence 68, Appl
47	21	67.7	201	4	US-10-060-255-69	Sequence 69, Appl
48	21	67.7	201	4	US-10-408-765A-717	Sequence 717, App
49	21	67.7	201	5	US-10-881-088-59	Sequence 59, Appl
50	21	67.7	201	5	US-10-881-088-68	Sequence 68, Appl
51	21	67.7	201	5	US-10-881-088-69	Sequence 69, Appl
52	21	67.7	201	5	US-10-287-436A-456	Sequence 456, App
53	21	67.7	201	5	US-10-287-436A-1258	Sequence 1258, Ap
54	21	67.7	201	6	US-11-264-096-2073	Sequence 2073, Ap
55	21	67.7	201	6	US-11-264-096-2075	Sequence 2075, Ap
56	21	67.7	201	6	US-11-264-096-2076	Sequence 2076, Ap
57	21	67.7	208	4	US-10-425-115-321090	Sequence 321090,
58	21	67.7	210	4	US-10-335-977-5883	Sequence 5883, Ap
59	21	67.7	210	4	US-10-335-977-5884	Sequence 5884, Ap
60	21	67.7	215	4	US-10-335-977-5885	Sequence 5885, Ap
61	21	67.7	233	4	US-10-424-599-165427	Sequence 165427,
62	21	67.7	238	4	US-10-282-122A-58562	Sequence 58562, A
63	21	67.7	271	5	US-10-667-295-98	Sequence 98, Appl
64	21	67.7	277	4	US-10-225-066A-370	Sequence 370, App
65	21	67.7	277	4	US-10-374-780A-2724	Sequence 2724, Ap
66	21	67.7	277	5	US-10-732-923-5393	Sequence 5393, Ap
67	21	67.7	277	5	US-10-225-066A-370	Sequence 370, App
68	21	67.7	277	5	US-10-667-295-97	Sequence 97, Appl

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 11, 2006, 22:56:56 ; Search time 151 Seconds  
(without alignments)  
2416.333 Million cell updates/sec

Title: US-10-072-159-11  
Perfect score: 708  
Sequence: 1 FSVGLEITYVTIPNMPPIRFTK.....YADNDNDSTFTGFLLYHDTN 130

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10072159/runat\_10082006\_161746\_24002/app\_query.fasta\_1  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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4	708	100.0	4517	3	US-09-776-976-5	Sequence 5, Appli	
5	708	100.0	4517	3	US-09-909-547-5	Sequence 5, Appli	
6	708	100.0	4517	4	US-10-231-814-5	Sequence 5, Appli	
7	708	100.0	4517	4	US-10-285-833-5	Sequence 5, Appli	
8	708	100.0	4545	3	US-09-569-852B-5	Sequence 5, Appli	
9	708	100.0	20966	3	US-09-776-976-7	Sequence 7, Appli	
10	708	100.0	20966	3	US-09-909-547-7	Sequence 7, Appli	
11	708	100.0	20966	3	US-09-569-852B-1	Sequence 1, Appli	
12	708	100.0	20966	4	US-10-231-814-7	Sequence 7, Appli	
13	708	100.0	20966	4	US-10-285-833-7	Sequence 7, Appli	
14	655	92.5	1276	2	US-08-463-911-1	Sequence 1, Appli	
15	655	92.5	1276	3	US-09-776-976-3	Sequence 3, Appli	
16	655	92.5	1276	3	US-09-909-547-3	Sequence 3, Appli	
17	655	92.5	1276	4	US-10-231-814-3	Sequence 3, Appli	
18	655	92.5	1276	4	US-10-285-833-3	Sequence 3, Appli	
19	645	91.1	1152	3	US-09-776-976-1	Sequence 1, Appli	
20	645	91.1	1152	3	US-09-909-547-1	Sequence 1, Appli	
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22	645	91.1	1152	4	US-10-285-833-1	Sequence 1, Appli	
23	287.5	40.6	3167	3	US-09-949-001-7	Sequence 7, Appli	
24	287.5	40.6	3198	3	US-09-949-001-2	Sequence 2, Appli	
25	287.5	40.6	10544	3	US-09-949-001-28	Sequence 28, Appl	
26	287.5	40.6	10544	3	US-09-949-001-33	Sequence 33, Appl	
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28	280.5	39.6	486	3	US-09-975-607A-1	Sequence 1, Appli	
29	270.5	38.2	2235	3	US-09-949-016-3736	Sequence 3736, Ap	
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33	266.5	37.6	1107	3	US-09-188-930-217	Sequence 217, App	
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37	265.5	37.5	1178	5	US-10-162-335-29	Sequence 29, Appl	
38	264	37.3	1839	2	US-08-383-744-1	Sequence 1, Appli	
39	264	37.3	1839	2	US-08-999-336-1	Sequence 1, Appli	
40	264	37.3	1839	7	PCT-US96-01427-1	Sequence 1, Appli	
41	254.5	35.9	4908	3	US-10-001-887-33	Sequence 33, Appl	
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45	248.5	35.1	1263	3	US-09-336-536-8	Sequence 8, Appli	

# ALIGNMENTS



GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 11, 2006, 23:26:35 ; Search time 174 Seconds  
(without alignments)  
1779.740 Million cell updates/sec

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Perfect score: 708  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
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2	708	100.0	819	8	US-11-297-169-1	Sequence 1, Appli	
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5	708	100.0	20966	9	US-11-390-954-1	Sequence 1, Appli	
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10	287.5	40.6	2065	8	US-11-266-748A-191588	Sequence 191588,	
11	287.5	40.6	3226	9	US-11-226-554-5	Sequence 5, Appli	
12	287.5	40.6	3226	9	US-11-248-718-5	Sequence 5, Appli	
13	287.5	40.6	3285	8	US-11-266-748A-29083	Sequence 29083, A	
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c 17	270.5	38.2	1000	8	US-11-266-748A-336658	Sequence 336658,	
18	270.5	38.2	1000	8	US-11-266-748A-395435	Sequence 395435,	
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21	268.5	37.9	991	8	US-11-266-748A-1291	Sequence 1291, Ap	
22	265.5	37.5	2395	8	US-11-266-748A-56243	Sequence 56243, A	
23	264.5	37.4	663	8	US-11-266-748A-41992	Sequence 41992, A	
c 24	257.5	36.4	671	8	US-11-266-748A-210109	Sequence 210109,	
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26	254.5	35.9	4443	8	US-11-266-748A-29582	Sequence 29582, A	
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c 32	243.5	34.4	1295	8	US-11-266-748A-135538	Sequence 135538,	
33	243.5	34.4	1377	8	US-11-296-092-41	Sequence 41, Appl	
34	243.5	34.4	1377	8	US-11-296-155-41	Sequence 41, Appl	
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c 37	219	30.9	924	8	US-11-266-748A-162394	Sequence 162394,	
38	219	30.9	1000	8	US-11-266-748A-293186	Sequence 293186,	
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45	214	30.2	547	8	US-11-266-748A-358887	Sequence 358887,	

#### ALIGNMENTS

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: August 11, 2006, 08:23:37 ; Search time 50 Seconds  
(without alignments)  
227.580 Million cell updates/sec

Title: US-10-072-159-11  
Perfect score: 708  
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Searched: 650591 seqs, 87530628 residues

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	708	100.0	130	2	US-10-060-845-11	Sequence 11, Appl
3	708	100.0	231	2	US-09-530-423-2	Sequence 2, Appli
4	708	100.0	244	1	US-08-463-911-7	Sequence 7, Appli
5	708	100.0	244	2	US-09-140-804-3	Sequence 3, Appli
6	708	100.0	244	2	US-09-336-536-20	Sequence 20, Appl
7	708	100.0	244	2	US-09-530-423-1	Sequence 1, Appli
8	708	100.0	244	2	US-09-686-838B-3	Sequence 3, Appli
9	708	100.0	244	2	US-09-911-176B-48	Sequence 48, Appl
10	708	100.0	244	2	US-09-552-225A-3	Sequence 3, Appli

11	708	100.0	244	2	US-09-619-740-51	Sequence 51, Appl
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14	708	100.0	244	2	US-09-569-852B-6	Sequence 6, Appli
15	708	100.0	244	2	US-09-552-204A-3	Sequence 3, Appli
16	708	100.0	244	2	US-10-621-787-3	Sequence 3, Appli
17	708	100.0	244	2	US-10-231-814-6	Sequence 6, Appli
18	708	100.0	244	2	US-10-285-833-6	Sequence 6, Appli
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22	655	92.5	247	2	US-09-140-804-8	Sequence 8, Appli
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24	655	92.5	247	2	US-09-506-855-3	Sequence 3, Appli
25	655	92.5	247	2	US-09-686-838B-8	Sequence 8, Appli
26	655	92.5	247	2	US-09-911-176B-3	Sequence 3, Appli
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28	655	92.5	247	2	US-09-776-976-4	Sequence 4, Appli
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30	655	92.5	247	2	US-09-909-547-4	Sequence 4, Appli
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36	645	91.1	247	2	US-09-776-976-2	Sequence 2, Appli
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39	645	91.1	247	2	US-10-285-833-2	Sequence 2, Appli
40	287.5	40.6	680	2	US-09-949-001-15	Sequence 15, Appl
41	287.5	40.6	680	2	US-09-949-001-20	Sequence 20, Appl
42	280.5	39.6	161	2	US-09-415-551-3	Sequence 3, Appli
43	280.5	39.6	161	2	US-09-975-607A-3	Sequence 3, Appli
44	270.5	38.2	744	2	US-09-949-016-9607	Sequence 9607, Ap
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#### ALIGNMENTS

##### RESULT 1

US-09-485-316A-11

; Sequence 11, Application US/09485316A

; Patent No. 6344441

; GENERAL INFORMATION:

; APPLICANT: Bihain, Bernard

; APPLICANT: Bougueleret, Lydie

; APPLICANT: Yen-Potin, Frances

; TITLE OF INVENTION: Lipoprotein-regulating medicaments

; FILE REFERENCE: GENSET.036APC

; CURRENT APPLICATION NUMBER: US/09/485,316A

; CURRENT FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: FR 97/10088

; PRIOR FILING DATE: 1997-08-06

; PRIOR APPLICATION NUMBER: FR 98/05032

; PRIOR FILING DATE: 1998-04-22

; PRIOR APPLICATION NUMBER: PCT IB98/01256

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 11, 2006, 08:35:41 ; Search time 33 Seconds  
(without alignments)  
265.169 Million cell updates/sec

Title: US-10-072-159-11  
Perfect score: 708  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	708	100.0	244	7	US-11-297-169-2	Sequence 2, Appli
3	708	100.0	244	7	US-11-390-954-6	Sequence 6, Appli
4	707	99.9	243	7	US-11-297-169-3	Sequence 3, Appli
5	661	93.4	244	7	US-11-297-169-5	Sequence 5, Appli
6	655	92.5	247	6	US-10-514-715-4	Sequence 4, Appli
7	655	92.5	247	7	US-11-297-169-4	Sequence 4, Appli
8	633	89.4	244	7	US-11-297-169-6	Sequence 6, Appli
9	615	86.9	240	7	US-11-297-169-7	Sequence 7, Appli

10	287.5	40.6	680	7	US-11-226-554-83	Sequence 83, Appl
11	287.5	40.6	680	7	US-11-248-718-83	Sequence 83, Appl
12	270.5	38.2	744	6	US-10-505-928-493	Sequence 493, App
13	243.5	34.4	243	7	US-11-296-092-42	Sequence 42, Appl
14	243.5	34.4	243	7	US-11-296-155-42	Sequence 42, Appl
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16	179.5	25.4	281	7	US-11-296-155-78	Sequence 78, Appl
17	156.5	22.1	259	6	US-10-196-749-62	Sequence 62, Appl
18	118.5	16.7	205	6	US-10-196-749-334	Sequence 334, App
19	98.5	13.9	316	7	US-11-147-397-42	Sequence 42, Appl
20	98.5	13.9	322	7	US-11-147-397-39	Sequence 39, Appl
21	98.5	13.9	350	7	US-11-147-397-41	Sequence 41, Appl
22	92	13.0	1904	6	US-10-537-642-1	Sequence 1, Appli
23	86	12.1	15	7	US-11-147-397-29	Sequence 29, Appl
24	74	10.5	370	6	US-10-953-349-16808	Sequence 16808, A
25	74	10.5	370	7	US-11-056-355B-53965	Sequence 53965, A
26	74	10.5	387	6	US-10-953-349-16807	Sequence 16807, A
27	74	10.5	387	7	US-11-056-355B-53964	Sequence 53964, A
28	71.5	10.1	183	6	US-10-528-104-2	Sequence 2, Appli
29	69.5	9.8	1160	7	US-11-192-046-250	Sequence 250, App
30	67.5	9.5	188	6	US-10-953-349-10085	Sequence 10085, A
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32	67.5	9.5	294	6	US-10-953-349-10083	Sequence 10083, A
33	67.5	9.5	552	6	US-10-509-131-50	Sequence 50, Appl
34	67.5	9.5	563	6	US-10-509-131-40	Sequence 40, Appl
35	67	9.5	362	7	US-11-330-403-18262	Sequence 18262, A
36	66.5	9.4	555	7	US-11-330-403-4956	Sequence 4956, Ap
37	66.5	9.4	2516	7	US-11-070-573-25	Sequence 25, Appl
38	66	9.3	216	7	US-11-056-355B-64569	Sequence 64569, A
39	66	9.3	262	7	US-11-056-355B-64568	Sequence 64568, A
40	65.5	9.3	663	7	US-11-056-355B-80630	Sequence 80630, A
41	65.5	9.3	666	7	US-11-056-355B-80629	Sequence 80629, A
42	65.5	9.3	670	7	US-11-056-355B-80628	Sequence 80628, A
43	65.5	9.3	2133	6	US-10-537-642-9	Sequence 9, Appli
44	64.5	9.1	549	7	US-11-330-403-8094	Sequence 8094, Ap
45	64	9.0	293	6	US-10-449-902-52122	Sequence 52122, A

#### ALIGNMENTS

##### RESULT 1

US-10-514-715-2

; Sequence 2, Application US/10514715

; Publication No. US20060166873A1

; GENERAL INFORMATION:

; APPLICANT: KADOWAKI, TAKASHI

; APPLICANT: YAMAUCHI, TOSHIMASA

; APPLICANT: KUBOTA, NAOTO

; APPLICANT: TERAUCHI, YASUO

; APPLICANT: KUBOTA, TETSUYA

; APPLICANT: NODA, TETSUO

; APPLICANT: NAGAI, RYOZO

; APPLICANT: IMAI, YASUSHI

; TITLE OF INVENTION: PREVENTIVE/REMEDY FOR ARTERIOSCLEROSIS

; FILE REFERENCE: 262193US0PCT

; CURRENT APPLICATION NUMBER: US/10/514,715

GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 11, 2006, 22:41:25 ; Search time 55.125 Seconds  
(without alignments)  
458.231 Million cell updates/sec

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Perfect score: 16  
Sequence: 1 XXFXGXLXX 9

Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Command line parameters:

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-LIST=1000 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=100  
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-HOST=abss08 -USER=US10072159 @CGN\_1\_1\_252 @runat\_10082006\_161645\_23320  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
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9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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c	2	16	100.0	17	3	US-09-371-772B-3897	Sequence 3897, Ap
c	3	16	100.0	17	3	US-09-685-664B-3897	Sequence 3897, Ap
c	4	16	100.0	17	5	US-10-138-674B-3897	Sequence 3897, Ap
c	5	16	100.0	18	2	US-08-379-081B-1	Sequence 1, Appli
c	6	16	100.0	18	2	US-08-379-081B-2	Sequence 2, Appli
c	7	16	100.0	18	2	US-08-379-081B-3	Sequence 3, Appli
c	8	16	100.0	18	2	US-08-379-081B-4	Sequence 4, Appli
c	9	16	100.0	18	2	US-08-379-081B-5	Sequence 5, Appli
c	10	16	100.0	18	2	US-08-379-081B-6	Sequence 6, Appli
c	11	16	100.0	18	2	US-08-379-081B-7	Sequence 7, Appli
c	12	16	100.0	18	2	US-08-379-081B-8	Sequence 8, Appli
c	13	16	100.0	18	2	US-08-379-081B-9	Sequence 9, Appli
c	14	16	100.0	18	2	US-08-379-081B-10	Sequence 10, Appl
c	15	16	100.0	18	2	US-08-379-081B-11	Sequence 11, Appl
c	16	16	100.0	18	2	US-08-379-081B-12	Sequence 12, Appl
c	17	16	100.0	18	2	US-08-379-081B-13	Sequence 13, Appl
c	18	16	100.0	18	2	US-08-379-081B-14	Sequence 14, Appl
c	19	16	100.0	18	2	US-08-379-081B-15	Sequence 15, Appl
c	20	16	100.0	18	2	US-08-379-081B-16	Sequence 16, Appl
c	21	16	100.0	18	2	US-08-379-081B-17	Sequence 17, Appl
c	22	16	100.0	18	2	US-08-379-081B-18	Sequence 18, Appl
c	23	16	100.0	18	2	US-08-379-081B-19	Sequence 19, Appl
c	24	16	100.0	18	2	US-08-379-081B-20	Sequence 20, Appl
c	25	16	100.0	18	2	US-08-379-078-1	Sequence 1, Appli
c	26	16	100.0	18	2	US-08-379-078-2	Sequence 2, Appli
c	27	16	100.0	18	2	US-08-379-078-3	Sequence 3, Appli
c	28	16	100.0	18	2	US-08-379-078-4	Sequence 4, Appli
c	29	16	100.0	18	2	US-08-379-078-5	Sequence 5, Appli
c	30	16	100.0	18	2	US-08-379-078-6	Sequence 6, Appli
c	31	16	100.0	18	2	US-08-379-078-7	Sequence 7, Appli
c	32	16	100.0	18	2	US-08-379-078-8	Sequence 8, Appli
c	33	16	100.0	18	2	US-08-379-078-9	Sequence 9, Appli
c	34	16	100.0	18	2	US-08-379-078-10	Sequence 10, Appl
c	35	16	100.0	18	2	US-08-379-078-11	Sequence 11, Appl
c	36	16	100.0	18	2	US-08-379-078-12	Sequence 12, Appl
c	37	16	100.0	18	2	US-08-379-078-13	Sequence 13, Appl
c	38	16	100.0	18	2	US-08-379-078-14	Sequence 14, Appl
c	39	16	100.0	18	2	US-08-379-078-15	Sequence 15, Appl
c	40	16	100.0	18	2	US-08-379-078-16	Sequence 16, Appl
c	41	16	100.0	18	2	US-08-379-078-17	Sequence 17, Appl
c	42	16	100.0	18	2	US-08-379-078-18	Sequence 18, Appl
c	43	16	100.0	18	2	US-08-379-078-19	Sequence 19, Appl
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	45	16	100.0	18	3	US-09-454-704A-1	Sequence 1, Appli
c	46	16	100.0	18	3	US-09-454-704A-3	Sequence 3, Appli
	47	16	100.0	18	3	US-09-454-704A-5	Sequence 5, Appli
	48	16	100.0	18	3	US-09-454-704A-6	Sequence 6, Appli
	49	16	100.0	18	3	US-09-454-704A-11	Sequence 11, Appl



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Run on: August 11, 2006, 08:01:40 ; Search time 10.125 Seconds  
 (without alignments)  
 77.805 Million cell updates/sec

Title: US-10-072-159-2  
 Perfect score: 16  
 Sequence: 1 XXFXGXLXX 9

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
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 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
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3	16	100.0	16	2	US-10-158-847-48	Sequence 48, Appl
4	16	100.0	16	2	US-10-158-825-48	Sequence 48, Appl
5	16	100.0	23	1	US-08-056-200-57	Sequence 57, Appl
6	16	100.0	23	1	US-08-056-200-58	Sequence 58, Appl
7	16	100.0	23	1	US-08-056-200-59	Sequence 59, Appl
8	16	100.0	23	1	US-08-800-644-57	Sequence 57, Appl
9	16	100.0	23	1	US-08-800-644-58	Sequence 58, Appl
10	16	100.0	23	1	US-08-800-644-59	Sequence 59, Appl

11	16	100.0	24	2	US-10-158-847-18	Sequence 18, Appl
12	16	100.0	24	2	US-10-158-825-18	Sequence 18, Appl
13	16	100.0	28	1	US-08-451-240-26	Sequence 26, Appl
14	16	100.0	28	1	US-08-451-240-36	Sequence 36, Appl
15	16	100.0	28	1	US-08-451-240-37	Sequence 37, Appl
16	16	100.0	28	1	US-08-470-846A-28	Sequence 28, Appl
17	16	100.0	28	1	US-08-470-846A-33	Sequence 33, Appl
18	16	100.0	28	2	US-09-154-390-28	Sequence 28, Appl
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20	16	100.0	28	2	US-09-154-390-41	Sequence 41, Appl
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23	16	100.0	28	5	PCT-US94-12591-37	Sequence 37, Appl
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28	16	100.0	44	2	US-08-471-970A-7	Sequence 7, Appli
29	16	100.0	44	2	US-09-723-677B-7	Sequence 7, Appli
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36	16	100.0	65	2	US-09-673-395A-337	Sequence 337, App
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38	16	100.0	65	2	US-09-978-303-9	Sequence 9, Appli
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45	16	100.0	73	2	US-09-651-150B-5	Sequence 5, Appli
46	16	100.0	75	1	US-08-783-395-2	Sequence 2, Appli
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48	16	100.0	75	2	US-09-716-129-73	Sequence 73, Appl
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52	16	100.0	92	2	US-09-134-000C-3938	Sequence 3938, Ap
53	16	100.0	98	2	US-09-214-095D-4	Sequence 4, Appli
54	16	100.0	98	2	US-09-940-727B-4	Sequence 4, Appli
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57	16	100.0	99	2	US-09-214-095D-92	Sequence 92, Appl
58	16	100.0	99	2	US-09-940-727B-88	Sequence 88, Appl
59	16	100.0	99	2	US-09-940-727B-92	Sequence 92, Appl
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62	16	100.0	100	2	US-09-940-727B-96	Sequence 96, Appl
63	16	100.0	100	2	US-10-104-047-2869	Sequence 2869, Ap
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65	16	100.0	103	2	US-09-489-039A-9077	Sequence 9077, Ap
66	16	100.0	103	2	US-09-134-000C-3515	Sequence 3515, Ap
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